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First Case of B.1.1.7 COVID-19 Variant Identified in Virginia

RICHMOND—The Virginia Department of Health (VDH) and the Department of General Services Division of Consolidated Laboratory Services (DCLS) today announced that the first case of the SARS-CoV-2 variant B.1.1.7 has been identified in a sample from an adult resident of Northern Virginia with no reported recent travel history. The B.1.1.7 variant, which first emerged in the United Kingdom in late 2020, is associated with increased person-to-person transmission of COVID-19.

DCLS confirmed the case using next-generation sequencing that provides a genetic blueprint of the virus that causes COVID-19. DCLS has informed the Centers for Disease Control and Prevention (CDC) of the case.

"Viruses change all the time, and we expect to see new strains as disease spreads," **said State Health Commissioner M. Norman Oliver, MD, MA**. "We know this variant strain spreads more quickly between people than other strains currently circulating in our communities, but we still have more to learn about whether it causes more severe illness. As our state public health officials closely monitor the emergence of the B.1.1.7 variant in our Commonwealth, it is important that all Virginians continue following mitigation measures."

In the United States, <u>nearly 200</u> cases of the B.1.1.7 variant have been detected in 23 states as of January 22, 2021. While scientists are working to better understand its impact on vaccine efficacy, early data suggests currently authorized vaccines are effective against the new variant. VDH continues to work with communities across Virginia to slow the spread of all strains of COVID-19 through widespread adherence to preventive measures, supporting testing and vaccination efforts, and conducting investigations of cases and outbreaks.

As a virus spreads from one person to another, it makes copies of itself and sometimes makes small genetic changes called mutations. Because of these mutations, new variants of a virus are expected to occur over time. According to the CDC, <u>multiple variants of the virus that causes COVID-19</u> have been documented in the United States and around the world. The B.1.1.7 variant contains an unusually large number of mutations.

DCLS began sequencing positive COVID-19 samples in March 2020, becoming one of the first public health labs in the nation to use this technology to examine the genetic makeup of the virus and track how it is changing and being transmitted in the Commonwealth. To date, DCLS has sequenced more than 10 percent of positive samples tested by the state lab, and is working with other labs in Virginia to solicit additional positive samples to sequence so public health officials can get a representation of variants circulating throughout Virginia.

"Sequencing is one of many tools we have available at the state's public health laboratory to enable medical and public health officials to quickly identify and respond to threats such as emerging COVID-19 variants," **said Dr. Denise Toney, Director of DCLS**. "We share this information not only within the Commonwealth, but with our federal and international partners to gain a better understanding of emerging genetic changes to SARS-CoV-2."

For more information about COVID-19 variants, visit the VDH COVID-19 Testing <u>website</u> and the CDC New COVID-19 Variants <u>website</u>. For more information on DCLS and its use of next-generation sequencing, visit <u>dgs.virginia.gov/dcls</u>.

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